

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/516, 587

Source: PCT

Date Processed by STIC: 12-22-04

# ***ENTERED***

**CRF Errors Edited by the STIC Systems  
Branch**

Serial Number: 10/516,587

CRF Edit Date: 12/22/04  
Edited by: re

     Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

     Corrected the SEQ ID NO. Sequence numbers edited were:

\_\_\_\_\_

     Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

\_\_\_\_\_

✓ Deleted: ✓ Invalid beginning/end-of-file text ;      page numbers

     Inserted mandatory headings/numeric identifiers, specifically:

\_\_\_\_\_

     Moved responses to same line as heading/numeric identifier, specifically:

\_\_\_\_\_

     Other:

\_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_



PCT

## RAW SEQUENCE LISTING

DATE: 12/22/2004

PATENT APPLICATION: US/10/516,587

TIME: 14:32:12

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\12202004\J516587.raw

```

4 <110> APPLICANT: KANEKA CORPORATION
6 <120> TITLE OF INVENTION: NOVEL ACYLASE GENE
8 <130> FILE REFERENCE: T719./ACYL-1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/516,587
C--> 10 <141> CURRENT FILING DATE: 2004-12-03
10 <150> PRIOR APPLICATION NUMBER: JP P2002-165722
11 <151> PRIOR FILING DATE: 2002-06-06
13 <160> NUMBER OF SEQ ID NOS: 15
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 2529
17 <212> TYPE: DNA
18 <213> ORGANISM: Stenotrophomonas maltophilia
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (126)...(2036)
24 <400> SEQUENCE: 1
25 tctacaacgg cttggcacat gtgccatcag tctaccccc aaagagcgca gaacgcaaag 60
27 cctgcacaca cttcacccgc cggggcagga gtacgcttgg gactttcctg cccgaggggt 120
29 cgtcc atg cat gtg cgt gcc gta gca gtt gcc atc gcc ctg agc ctg tcc 170
30 Met His Val Arg Ala Val Ala Val Ala Ile Ala Leu Ser Leu Ser
31 1 5 10 15
33 agc acc gtg ctg gcc gcc gac acc ccg ccg atg acc ccg gac atc agc 218
34 Ser Thr Val Leu Ala Ala Asp Thr Pro Pro Met Thr Pro Asp Ile Ser
35 20 25 30
39 ggc aag cct ttc att gcg ccc gat gtc ggc cgc gac tac gac aag cgc 266
40 Gly Lys Pro Phe Ile Ala Pro Asp Val Gly Arg Asp Tyr Asp Lys Arg
41 35 40 45
43 gtg gtg atg gtg ccg atg cgc gac ggt acc agg ctg tac acg gtg atc 314
44 Val Val Met Val Pro Met Arg Asp Gly Thr Arg Leu Tyr Thr Val Ile
45 50 55 60
47 gtg gtg ccc aag ggc gcg cac aat gcc ccg atc ctg ctg acc cgc acg 362
48 Val Val Pro Lys Gly Ala His Asn Ala Pro Ile Leu Leu Thr Arg Thr
49 65 70 75
51 ccc tac gat gct gcc ggc cgc gcc agc cgc agc gat tcg ccg cgc atg 410
52 Pro Tyr Asp Ala Ala Gly Arg Ala Ser Arg Ser Asp Ser Pro Arg Met
53 80 85 90 95
55 cgc gac ctg ctg ccg cag ggg gat gaa gtc ttc gtc gat ggc ggc tat 458
56 Arg Asp Leu Leu Pro Gln Gly Asp Glu Val Phe Val Asp Gly Gly Tyr
57 100 105 110
59 atc cgc gtg ttc cag gac atc cgg ggc aag tac ggt tcg gaa ggc gat 506
60 Ile Arg Val Phe Gln Asp Ile Arg Gly Lys Tyr Gly Ser Glu Gly Asp
61 115 120 125
63 tat gtg atg acc cgg ccg ctg cgc ggg ccg ttg aac aac acc aag gtc 554

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```

64 Tyr Val Met Thr Arg Pro Leu Arg Gly Pro Leu Asn Asn Thr Lys Val
65          130          135          140
67 gac cac tcc acc gat gca tgg gac acc atc gac tgg ttg gtg aaa cac    602
68 Asp His Ser Thr Asp Ala Trp Asp Thr Ile Asp Trp Leu Val Lys His
69      145          150          155
71 gtg ccg gaa agc aac ggc aag gtc ggc atg ctg ggc tcg tcg tac gaa    650
72 Val Pro Glu Ser Asn Gly Lys Val Gly Met Leu Gly Ser Ser Tyr Glu
75 160          165          170          175
77 ggc ttc acc gtg gtg atg gcc ctg acc gac ccg cat ccg gcg ctg aag    698
78 Gly Phe Thr Val Val Met Ala Leu Thr Asp Pro His Pro Ala Leu Lys
79          180          185          190
81 gtg gcc gcc ccg cag agc ccg atg gtc gat ggc tgg atg ggc gac gac    746
82 Val Ala Ala Pro Gln Ser Pro Met Val Asp Gly Trp Met Gly Asp Asp
83          195          200          205
85 tgg ctc aac tac ggg gcc ttc cgc cag gtc aat ttc aac tac ttc gca    794
86 Trp Leu Asn Tyr Gly Ala Phe Arg Gln Val Asn Phe Asn Tyr Phe Ala
87      210          215          220
89 atg cag acc gag aag cgc ggc aag ggc acg ccg ctg ccc agc ctg ggc    842
90 Met Gln Thr Glu Lys Arg Gly Lys Gly Thr Pro Leu Pro Ser Leu Gly
91      225          230          235
93 tac gac gac tac agc acc ttc ctg cgc atc ggt tcg gcc ggt gac tac    890
94 Tyr Asp Asp Tyr Ser Thr Phe Leu Arg Ile Gly Ser Ala Gly Asp Tyr
95 240          245          250          255
97 gca cgc ttc acc ggc gtg gac cag ctg acc tgg tgg aag aag ctg gtg    938
98 Ala Arg Phe Thr Gly Val Asp Gln Leu Thr Trp Trp Lys Lys Leu Val
99          260          265          270
101 cag cac ccg gcc tac gat ggc ttc tgg cag ggc cag gcg ctg gat gcg    986
102 Gln His Pro Ala Tyr Asp Gly Phe Trp Gln Gly Gln Ala Leu Asp Ala
103          275          280          285
105 gtg atg gcg aag acc ccg ctg aag gtg ccg acc atg tgg ctg cag ggc    1034
106 Val Met Ala Lys Thr Pro Leu Lys Val Pro Thr Met Trp Leu Gln Gly
107      290          295          300
109 ctg tgg gac cag gaa gac atg tgg ggc gcc aac cat gcc tac cag gcg    1082
112 Leu Trp Asp Gln Glu Asp Met Trp Gly Ala Asn His Ala Tyr Gln Ala
113      305          310          315
115 atg gaa ggc cgc gac acc ggc aat acc cac aat tac ctg gtg atg ggc    1130
116 Met Glu Gly Arg Asp Thr Gly Asn Thr His Asn Tyr Leu Val Met Gly
117 320          325          330          335
119 ccg tgg cgg cac agc cag gtg aac tac acc ggc aac gag ctg ggt gcg    1178
120 Pro Trp Arg His Ser Gln Val Asn Tyr Thr Gly Asn Glu Leu Gly Ala
121          340          345          350
123 ctg aag ttc gag ggc gat acc gcg ctg cag ttc cgc cgc gat gtg ctc    1226
124 Leu Lys Phe Glu Gly Asp Thr Ala Leu Gln Phe Arg Arg Asp Val Leu
125          355          360          365
127 aag ccg ttc ttc gac cag tac ctg gtg gat ggc gca ccg aag gcc gac    1274
128 Lys Pro Phe Phe Asp Gln Tyr Leu Val Asp Gly Ala Pro Lys Ala Asp
129      370          375          380
131 acg ccg ccg gtg ctc atc tac aac acc ggc gaa aac cac tgg gat cgc    1322
132 Thr Pro Pro Val Leu Ile Tyr Asn Thr Gly Glu Asn His Trp Asp Arg

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```

133      385      390      395
135 ctg cag ggc tgg ccg cgc agt tgc gac aag ggc tgc acg gcg gcc agc 1370
136 Leu Gln Gly Trp Pro Arg Ser Cys Asp Lys Gly Cys Thr Ala Ala Ser
137 400      405      410      415
139 aag ccg ctg tac ctg cgt gcc ggt ggc aag ctg gcc ttc cag gca ccg 1418
140 Lys Pro Leu Tyr Leu Arg Ala Gly Gly Lys Leu Ala Phe Gln Ala Pro
141      420      425      430
143 gcg gcg ggt gaa ggt gat ttc gag gaa tac gtg tcc gac ccg gcc aag 1466
144 Ala Ala Gly Glu Gly Asp Phe Glu Glu Tyr Val Ser Asp Pro Ala Lys
145      435      440      445
149 ccg gtg ccg ttc gtg ccg cgc ccg gtg cgt ttt ggc gac cgt gac atg 1514
150 Pro Val Pro Phe Val Pro Arg Pro Val Arg Phe Gly Asp Arg Asp Met
151      450      455      460
153 tgg acc acg tgg ctg gtg aag gac caa cgt ttt gtc gat ggt cgt ccg 1562
154 Trp Thr Thr Trp Leu Val Lys Asp Gln Arg Phe Val Asp Gly Arg Pro
155      465      470      475
157 gat gtg ctg acc ttc atc acc gaa ccg ctg gcc gag ccg ctg cgg atc 1610
158 Asp Val Leu Thr Phe Ile Thr Glu Pro Leu Ala Glu Pro Leu Arg Ile
159 480      485      490      495
161 ggc ggc gcg ccg gtg gtg cat ctg cag gcg tcc acc agt ggc acc gac 1658
162 Gly Gly Ala Pro Val Val His Leu Gln Ala Ser Thr Ser Gly Thr Asp
163      500      505      510
165 agc gac tgg gtg gtg aag ctg atc gac gtc tac ccg gat cag gaa gcg 1706
166 Ser Asp Trp Val Val Lys Leu Ile Asp Val Tyr Pro Asp Gln Glu Ala
167      515      520      525
169 tca acg ccg gaa atg ggt ggc tat gag ctg ccg gtg tcc ctg gcg atc 1754
170 Ser Thr Pro Glu Met Gly Gly Tyr Glu Leu Pro Val Ser Leu Ala Ile
171      530      535      540
173 ttc cgt ggg cgc tat cgg gag agt ttc agc gac ccg aag ccg ctg gca 1802
174 Phe Arg Gly Arg Tyr Arg Glu Ser Phe Ser Asp Pro Lys Pro Leu Ala
175      545      550      555
177 gcg aac cag gtg ctg ccg tac cgc ttt gat ctg ccc aat gcc aac cat 1850
178 Ala Asn Gln Val Leu Pro Tyr Arg Phe Asp Leu Pro Asn Ala Asn His
179 560      565      570      575
181 gtg ttc cag aag ggg cac cgg gtg atg gtg cag gtg cag tcc agc ctg 1898
182 Val Phe Gln Lys Gly His Arg Val Met Val Gln Val Gln Ser Ser Leu
183      580      585      590
187 ttc ccg ctg tat gac cgc aac ccg cag acc tac gtg ccg aac atc tac 1946
188 Phe Pro Leu Tyr Asp Arg Asn Pro Gln Thr Tyr Val Pro Asn Ile Tyr
189      595      600      605
191 ctg gcc aag ccg ggc gat tac cag aag gcc acg cag ccg gtg tgg cac 1994
192 Leu Ala Lys Pro Gly Asp Tyr Gln Lys Ala Thr Gln Arg Val Trp His
193      610      615      620
195 agc gcc gcg cag gcg agc tac gtc gac ctg ccg gtg tac tga 2036
196 Ser Ala Ala Gln Ala Ser Tyr Val Asp Leu Pro Val Tyr
197      625      630      635
199 ggcggagaat ggcgtggtag tgccggccgc tggccggcaa cgccggagcgg tagcgcgggg 2096
201 ccatgccccg cggatggggg agtgccggcc gctggccggc aacgcgggtga agccggcgcg 2156
203 tgtcgaccaa ggccgacacc tgccagagca cgtcagccta ccttcgaggg accggtgcgc 2216

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```

205 cagcggctgg gaaccagacc gaagcgcttg cggaaggcgg cggcgaagtt gctgggggtgg 2276
207 cggtagccgg tggcgccgc cgctgttca acgctccagc cgtgttcgcg caggccgcgt 2336
209 tcggcggttg gcatgcgttg ttcgtgcagg tagtcgaaca ccgagcaccg gtattgctgc 2396
211 acgaagtggc ggcgagcga gctgggactc atgcaggcca gctgggccag ttccaccagg 2456
213 ctgtgggcgt ggctgggacg gtcgtgcagg aagccccgca cgcgttcaat cgggccaaagt 2516
215 tggccgcgcc aaa 2529
218 <210> SEQ ID NO: 2
219 <211> LENGTH: 636
220 <212> TYPE: PRT
223 <213> ORGANISM: Stenotrophomonas maltophilia
225 <400> SEQUENCE: 2
226 Met His Val Arg Ala Val Ala Val Ala Ile Ala Leu Ser Leu Ser Ser
227 1 5 10 15
228 Thr Val Leu Ala Ala Asp Thr Pro Pro Met Thr Pro Asp Ile Ser Gly
229 20 25 30
230 Lys Pro Phe Ile Ala Pro Asp Val Gly Arg Asp Tyr Asp Lys Arg Val
231 35 40 45
232 Val Met Val Pro Met Arg Asp Gly Thr Arg Leu Tyr Thr Val Ile Val
233 50 55 60
234 Val Pro Lys Gly Ala His Asn Ala Pro Ile Leu Leu Thr Arg Thr Pro
235 65 70 75 80
236 Tyr Asp Ala Ala Gly Arg Ala Ser Arg Ser Asp Ser Pro Arg Met Arg
237 85 90 95
238 Asp Leu Leu Pro Gln Gly Asp Glu Val Phe Val Asp Gly Gly Tyr Ile
239 100 105 110
240 Arg Val Phe Gln Asp Ile Arg Gly Lys Tyr Gly Ser Glu Gly Asp Tyr
241 115 120 125
242 Val Met Thr Arg Pro Leu Arg Gly Pro Leu Asn Asn Thr Lys Val Asp
243 130 135 140
244 His Ser Thr Asp Ala Trp Asp Thr Ile Asp Trp Leu Val Lys His Val
245 145 150 155 160
246 Pro Glu Ser Asn Gly Lys Val Gly Met Leu Gly Ser Ser Tyr Glu Gly
247 165 170 175
248 Phe Thr Val Val Met Ala Leu Thr Asp Pro His Pro Ala Leu Lys Val
249 180 185 190
250 Ala Ala Pro Gln Ser Pro Met Val Asp Gly Trp Met Gly Asp Asp Trp
251 195 200 205
252 Leu Asn Tyr Gly Ala Phe Arg Gln Val Asn Phe Asn Tyr Phe Ala Met
253 210 215 220
254 Gln Thr Glu Lys Arg Gly Lys Gly Thr Pro Leu Pro Ser Leu Gly Tyr
255 225 230 235 240
256 Asp Asp Tyr Ser Thr Phe Leu Arg Ile Gly Ser Ala Gly Asp Tyr Ala
257 245 250 255
258 Arg Phe Thr Gly Val Asp Gln Leu Thr Trp Trp Lys Lys Leu Val Gln
259 260 265 270
260 His Pro Ala Tyr Asp Gly Phe Trp Gln Gly Gln Ala Leu Asp Ala Val
261 275 280 285
262 Met Ala Lys Thr Pro Leu Lys Val Pro Thr Met Trp Leu Gln Gly Leu
263 290 295 300

```

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```

264 Trp Asp Gln Glu Asp Met Trp Gly Ala Asn His Ala Tyr Gln Ala Met
265 305 310 315 320
266 Glu Gly Arg Asp Thr Gly Asn Thr His Asn Tyr Leu Val Met Gly Pro
267 325 330 335
268 Trp Arg His Ser Gln Val Asn Tyr Thr Gly Asn Glu Leu Gly Ala Leu
269 340 345 350
270 Lys Phe Glu Gly Asp Thr Ala Leu Gln Phe Arg Arg Asp Val Leu Lys
271 355 360 365
272 Pro Phe Phe Asp Gln Tyr Leu Val Asp Gly Ala Pro Lys Ala Asp Thr
273 370 375 380
274 Pro Pro Val Leu Ile Tyr Asn Thr Gly Glu Asn His Trp Asp Arg Leu
275 385 390 395 400
276 Gln Gly Trp Pro Arg Ser Cys Asp Lys Gly Cys Thr Ala Ala Ser Lys
277 405 410 415
278 Pro Leu Tyr Leu Arg Ala Gly Gly Lys Leu Ala Phe Gln Ala Pro Ala
279 420 425 430
280 Ala Gly Glu Gly Asp Phe Glu Glu Tyr Val Ser Asp Pro Ala Lys Pro
281 435 440 445
282 Val Pro Phe Val Pro Arg Pro Val Arg Phe Gly Asp Arg Asp Met Trp
283 450 455 460
284 Thr Thr Trp Leu Val Lys Asp Gln Arg Phe Val Asp Gly Arg Pro Asp
285 465 470 475 480
286 Val Leu Thr Phe Ile Thr Glu Pro Leu Ala Glu Pro Leu Arg Ile Gly
287 485 490 495
288 Gly Ala Pro Val Val His Leu Gln Ala Ser Thr Ser Gly Thr Asp Ser
289 500 505 510
290 Asp Trp Val Val Lys Leu Ile Asp Val Tyr Pro Asp Gln Glu Ala Ser
291 515 520 525
292 Thr Pro Glu Met Gly Gly Tyr Glu Leu Pro Val Ser Leu Ala Ile Phe
293 530 535 540
294 Arg Gly Arg Tyr Arg Glu Ser Phe Ser Asp Pro Lys Pro Leu Ala Ala
295 545 550 555 560
296 Asn Gln Val Leu Pro Tyr Arg Phe Asp Leu Pro Asn Ala Asn His Val
297 565 570 575
298 Phe Gln Lys Gly His Arg Val Met Val Gln Val Gln Ser Ser Leu Phe
299 580 585 590
300 Pro Leu Tyr Asp Arg Asn Pro Gln Thr Tyr Val Pro Asn Ile Tyr Leu
301 595 600 605
302 Ala Lys Pro Gly Asp Tyr Gln Lys Ala Thr Gln Arg Val Trp His Ser
303 610 615 620
304 Ala Ala Gln Ala Ser Tyr Val Asp Leu Pro Val Tyr
305 625 630 635
308 <210> SEQ ID NO: 3
309 <211> LENGTH: 25
310 <212> TYPE: PRT
311 <213> ORGANISM: Stenotrophomonas maltophilia
313 <220> FEATURE:
314 <221> NAME/KEY: PEPTIDE
315 <222> LOCATION: (1)...(25)

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/516,587

DATE: 12/22/2004

TIME: 14:32:13

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\12202004\J516587.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date